



6297.101.0721.txt
SEQUENCE LISTING

Lowery, David E.
Smith, Valdin G.
Kubiak, Teresa M.
Larsen, Martina J.

4110 Drosophila 3 Protein Coupled Receptors, Nucleic Acids, And Methods Related To The Same

4130 6297.lcp

4140 09/693,746

4141 2000-10-20

4150 09/425,676

4151 1999-10-22

4160 163

4170 PatentIn version 3.1

4210 1

4211 1803

4212 DNA

4213 D. melanogaster

4400 1

```
atggccaact taagctggct gaggaccatc accaccacct cctcctccat cagcaccagc      60
cagctgccat tggtcagcac aaccaactgg agcctaacgt cgcggggaac tactagcgct      120
atcttgggcg atgtggctgc atcggatgag gataggagcg gggggatcat tcacaaccag      180
ctcgtgcaca tctctctcta cgtctctgac gcacgggtct ttgtcctggg tgtcttcgga      240
aatgtcctgg ttgtctacgt agttctgagg aatcggggca tgcagactgt gaccaatata      300
ctcatcacga atctggccct gtggacata ttgtctgag tctggcggtt gcattttact      360
cagctttaca cgttcctggg tctgtgggca ttgggagga gtctgtgcaa tctggtgtcc      420
tttgccacag gatgcagcat ctacatctcc acgtcgaccc tcacctcgat tgcctatgat      480
cggtaacttg ttatcatata ccccttccat cggcgatga agctctccac ctgcatcggg      540
atcatagtga gcattctggg gatagccttg ctggcaccg ttccctaagg catgtacatg      600
aagatgacca acgagctggg gaaagggaag cagacaggca acgagacct ggtggaggcc      660
actctaattg taaaagggaag ctttctgggc cagggatcag gattcatcga ggcgccggac      720
ctaacctcgg ccacccacgg ctatatgag gtgatgaac cgggatcaac gggacccggag      780
atgcccctat tgggggtgta ctgagaggag aactggccat cggagcagta ccggaagggtg      840
ctcggtgcaa tcacaaccac tctgagttt gtgctgccc tcttcacat ctgatttgc      900
cacgtgtgga tatcggtgaa gctaaaccag cgggcbaggg ccaagccggg atcgaaatcc      960
tcgagacggg aggagcggga tcgggatcgc aagaaccgca ccaaccgcat gctcatcgcc      1020
atgggtggcg tattgggact cagctggctg cccatcaatg tggtaaacat attogatgac      1080
ttcgatgaca agtcacaaga gtggcgcttc tacatccat tctctcttgt ggccactct      1140
```


0287.108.3724.txt

attgccatga gctccacctg ctacautccc ttcctgtacg cctgggtgaa cgaagaattc 1200
 cgcgaaggagt tcaagcactg gctgccttcc tttcaatccct cgaacaacaa cctcattaac 1260
 atcaccaggg gctataatcg cagtgatcgg aacacctgtg gtcgcgagct gcatacatggc 1320
 aaggggggatg gtggcattgg cgggtggpact ctggagcgcc agaacacgga cgaacaacgc 1380
 atcaccacgg agacctgtct gcccgaaggag aagctgtgta ttatcccccag ggaacggact 1440
 tacggcaatg gcacggggcg cgtgtcgcca atccttagcg ggcggggcat taacgcgcgc 1500
 ctgggtgcacg gtggcgacca tcagatgcac cagctgcagc cgtcacacca tcaacaggtg 1560
 gagctgaaga ggcaatccg ccggcggaca gacgagacgg acgggggatta cctggactcc 1620
 ggcgacgagc agacctgtga ggtgcgcttc agcgagacgc cgttcgtcag caccgataat 1680
 accacccggga tcagcattct ggagacgagt acgagtcact ggcaggactc ggatgtgatg 1740
 gtgcagctgg ggcaggcaat cggcgcgggt ggtggggcag agctggggag gogaatcaac 1800
 tga 1803

0210 - 2
 0211 - 600
 0212 - PPT
 0213 - D. melanogaster

0400 - 2

Met Ala Asn Leu Ser Trp Leu Ser Thr Ile Thr Thr Thr Ser Ser Ser
 1 5 10 15

Ile Ser Thr Ser Gln Leu Pro Leu Val Ser Thr Thr Asn Trp Ser Leu
 20 25 30

Thr Ser Pro Gly Thr Thr Ser Ala Ile Leu Ala Asp Val Ala Ala Ser
 35 40 45

Asp Glu Asp Arg Ser Gly Gly Ile Ile His Asn Gln Phe Val Gln Ile
 50 55 60

Phe Phe Tyr Val Leu Tyr Ala Thr Val Phe Val Leu Gly Val Phe Gly
 65 70 75 80

Asn Val Leu Val Cys Tyr Val Val Leu Arg Asn Arg Ala Met Gln Thr
 85 90 95

Val Thr Asn Ile Phe Ile Thr Asn Leu Ala Leu Ser Asp Ile Leu Leu
 100 105 110

Cys Val Leu Ala Val Pro Phe Thr Pro Leu Tyr Thr Phe Met Gly Arg
 115 120 125

Trp Ala Phe Gly Arg Ser Leu Cys His Leu Val Ser Phe Ala Gln Gly


```

131      135      141
Cys Ser Ile Tyr Ile Ser Thr Leu Thr Leu Thr Ser Ile Ala Ile Asp
145      151      158
Arg Tyr Phe Val Ile Ile Tyr Pro Phe His Pro Arg Met Lys Leu Ser
165      170      175
Thr Cys Ile Gly Ile Ile Val Ser Ile Trp Val Ile Ala Leu Leu Ala
180      185      190
Thr Val Pro Tyr Gly Met Tyr Met Lys Met Thr Asn Glu Leu Val Asn
195      200      205
Gly Thr Gln Thr Gly Asn Glu Thr Leu Val Glu Ala Thr Leu Met Leu
210      215      220
Asn Gly Ser Phe Val Ala Gln Gly Ser Gly Phe Ile Glu Ala Pro Asp
225      230      235      240
Ser Thr Ser Ala Thr Gln Ala Tyr Met Gln Val Met Thr Ala Gly Ser
245      250      255
Thr Gly Pro Glu Met Pro Tyr Val Arg Val Tyr Cys Glu Glu Asn Trp
260      265      270
Pro Ser Glu Gln Tyr Arg Lys Val Phe Gly Ala Ile Thr Thr Thr Leu
275      280      285
Gln Phe Val Leu Pro Phe Phe Ile Ile Ser Ile Cys Tyr Val Trp Ile
290      295      300
Ser Val Lys Leu Asn Gln Arg Ala Arg Ala Lys Pro Gly Ser Lys Ser
305      310      315      320
Ser Arg Arg Glu Glu Ala Asp Arg Asp Arg Lys Lys Arg Thr Asn Arg
325      330      335
Met Leu Ile Ala Met Val Ala Val Phe Gly Leu Ser Trp Leu Pro Ile
340      345      350
Asn Val Val Asn Ile Phe Asp Asp Phe Asp Asp Lys Ser Asn Glu Trp
355      360      365
Arg Phe Tyr Ile Leu Phe Phe Phe Val Ala His Ser Ile Ala Met Ser
370      375      380
Ser Thr Cys Tyr Asn Pro Phe Leu Tyr Ala Trp Leu Asn Glu Asn Phe
385      390      395      400

```


Arg Lys Glu Ile Lys His Val Leu Pro Cys Ile Asn Pro Ser Asn Asn
411 411 411

Asn Ile Ile Asn Ile Thr Arg Gly Tyr Asn Arg Ser Asp Arg Asn Thr
420 420 420

Cys Gly Pro Arg Leu His His Gly Lys Gly Asp Gly Gly Met Gly Gly
435 435 440 445

Gly Ser Leu Asp Ala Asp Asp Gln Asp Glu Asn Gly Ile Thr Gln Glu
450 455 460

Thr Cys Leu Pro Lys Glu Lys Leu Leu Ile Ile Pro Arg Glu Pro Thr
465 470 475 480

Tyr Gly Asn Gly Thr Gly Ala Val Ser Pro Ile Leu Ser Gly Arg Gly
485 490 495

Ile Asn Ala Ala Leu Val His Gly Gly Asp His Gln Met His Gln Leu
500 505 510

Gln Pro Ser His His Gln Gln Val Glu Leu Thr Arg Arg Ile Arg Arg
515 520 525

Arg Thr Asp Glu Thr Asp Gly Asp Tyr Leu Asp Ser Gly Asp Glu Gln
530 535 540

Thr Val Glu Val Arg Phe Ser Glu Thr Pro Phe Val Ser Thr Asp Asn
545 550 555 560

Thr Thr Gly Ile Ser Ile Leu Glu Thr Ser Thr Ser His Cys Gln Asp
565 570 575

Ser Asp Val Met Val Glu Leu Gly Glu Ala Ile Gly Ala Gly Gly Gly
580 585 590

Ala Glu Leu Gly Arg Arg Ile Asn
595 600

02100 3
02110 1445
02120 DNA
02130 D. melanogaster

04000 3
atgaatcaga cggagccccc ccagctggca gatggggagg atctgagtggt atagccagc 6
aggagcaaca ggggtgggta tctggacgag cggcaccgca tggactacct tgaactgggg 12
tcgggtgcag cctgaacac tactggcacc aagacctcgg atctgaatga tactgggagg 18

0237.105.0101.txt

```

aggcggctgg agcgggtgat tatcgatagg ttctcgagca aagggggggt ggaacggcgc 240
tggtaaccac ttctcactag catgtacagg gtgataatag tcttgggggc cctagggcgc 300
aacctgggttg ctatagccgt catccggaag ccctacatgc gcaatgctag caatctgttc 360
atctccacac tggccatata gtaactact ttatgcatag tcaacatgac gctgaccttg 420
atggagatcc tgtccaagta ctggccctac ggcctctgct ccctcctgtg caaacagatt 480
gcaatgctgc aggcactctg tttttctgtg tcgacaatat ccataacggc cattgcttc 540
gacagatata aggtgatcgt gtacccacag cgggacagcc tgcagttcgt gggcgcggtg 600
acgatccttg cggggatctg ggcactggca ctgctgctgg ctgcgcctgt gttcgtctac 660
aaggagctga tcaacacaga cagccgggca ctctgcagc agatcggcct gcaggacag 720
atcccgtaac gaattgagga ctggccaagt cgcaacgggc gcttctacta ctgcacttc 780
tggctgttgg tacaatacct ggtgccacac ctgacgtctt cgggtggcata cttcgggcat 840
tacaacaagg tgaagagcgc catcaccttg gtgctctgac aggcgtcttc cgtccagcgg 900
aaggtgggag gggggcggtg gatgaagcgc accaactgcc tactgatcag catcgccatc 960
atctctgggg tttcttggct gcgcgtgaac ttttcaaac tgtacgggga catggagcgc 1020
tcgctgggtc ctcagagcat gctagtccgc tacgccatct gccacatgat cggcatgagc 1080
tcgctctgct ccaacccgtt gctctacggc tggctcaacg acaacttcgc taaagaattt 1140
caagaaactgc tctgccttg ctcagacact aatgttgcct ttaacgggta cagcacagc 1200
tgcacgtcc aggcggcggc gcgcaagcgt cgcaagttag gcgcgaact ctccaaaggc 1260
gaactcaagg tgcctggggc aggggggggc cagagcggta cggcggggg ggaaggcgg 1320
ctggagggca ccgaactcat gacgggcac cagcggggg gactgcgcag cgcataaac 1380
gagtgggttg cctccagga ccacaacccc gtgcctcgg aggtcaccaa gctgatgcgc 1440
cggtc 1445

```

0210 4
 0211 397
 0212 PRT
 0213 D. melanogaster

0400 4

Met Glu Asn Thr Thr Met Leu Ala Asn Ile Ser Leu Asn Ala Thr Arg
 1 5 10 15

Asn Glu Glu Asn Ile Thr Ser Phe Phe Thr Asp Glu Glu Trp Leu Ala
 20 25 30

Ile Asn Gly Thr Leu Pro Trp Ile Val Gly Phe Phe Phe Gly Val Ile
 35 40 45

039011F.JUL81.txt

Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val
50 55 60

Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu
65 70 75 80

Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Phe Phe Thr Ala
85 90 95

Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg
100 105 110

Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
115 120 125

Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile
130 135 140

Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val
145 150 155 160

Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
165 170 175

His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
180 185 190

Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
195 200 205

Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
210 215 220

Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
245 250 255

Leu Val Val Val Val Val Ile Ala Phe Ala Ser Leu Trp Leu Pro Val
260 265 270

Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
275 280 285

Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
290 295 300

Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe

315

315

315

315

Arg Lys Ala Phe Tyr Lys Ala Val Asn Gln Ser Ser Ser Arg Tyr Ala Asn
315 315 315

Tyr Thr Ser Asp Leu Phe Phe Phe Arg Lys Thr Ser Gln Ala Arg Thr
340 340 340 340 340

Ser Thr Thr Gly Leu
355

1210> 5
1211> 1376
1212> DNA
1213> D. melanogaster

1400> 5
atgaatcaga cggagccccc ccagctggca gatggggagg atctgagtgg atacgcacag 60
aggagcaaca ggggtgggta tctggacgac cggcaccgcc tggactacct tgcctggggc 120
agggtgcacg cccccaacac cactgcacac aacacccgcc atctgaatga gactggggagc 180
aggccgctgg accgggtggt tatcgatagg tctctgagca acagggcggg ggacagcccc 240
tggtaaccac tgcacacag catgtacggc gtgctaatac tcttcggggc cctaggcaac 300
accctgggtg ttatagccgt catccgggaag cccatcatgc gcaatgctcg caatctgttc 360
atctcaacc tggccatata ggacccactt ttatgcctag tcaacatgcc gctgaccttg 420
atggagatcc tgtccaagta ctggccctac ggccctctgt ccatctgttg caaaacgatt 480
cccatgctgc aggcaccttg tattctcttg tgcacaatat ccataacggc cattgcttcc 540
gacagatata aggtgatcgt gtaccccaac cgggacagcc tgcagttcgt gggcgcggtg 600
acgatccctg cggggatctg ggcactggca ctgctgctgg cctcgccgct gttcgtctac 660
aaggagctga tcaaacacga cagcccgga ctctgcagc agatcgccct gcagagacag 720
atccgtact gcattgagga ctggccaaat cgcacacggc gcttctacta ctgatcttc 780
tcgctgtgag tacaataact ggtgcacata ctgatctct cggtggcata cttcgggata 840
tacaacaaag tgaagagccg catcacctg gtgctgtgag aggcgtcttc cgtcagcgg 900
aaggtggagc gggggcgccg gatgaagcgc accaactgcc tactgatcag catcgccatc 960
atctctggcg tttcttgggt gccgtgaa ttttcaacc tgtacggga catggagcgc 1020
tcgccggtca ctacagagca gctagtccgc taccacatct gctacatgat cggcatgagc 1080
tcgccctgct ccaaccggtt gctctacggc tgggtcaacg acaacttcg ctgcaacgct 1140
caggcggcgg cggcgaagcg tgcgaagttg gggcgcgaac tctccaaagg cgaactcaag 1200
ctgctggggc caggcggcgc ccagagcggg accgcggcgg ggggaaggcg tctggcgggc 1260
accgaattca tgaacgacac cctcagggag ggaattcgca ggcacataac cgaatgggta 1320

Page 6

4287.101.F1a1.txt

Asn Thr Asp Thr Pro Ala Leu Leu Gln Gln Ile Gly Leu Gln Asp Thr
215 230 235 240

Ile Pro Tyr Cys Ile Gln Asp Trp Pro Ser Arg Asn Gly Arg Phe Tyr
245 260 265

Tyr Ser Ile Phe Ser Leu Cys Val Gln Tyr Leu Val Pro Ile Leu Ile
265 280 285

Val Ser Val Ala Tyr Phe Gly Ile Tyr Asn Lys Leu Lys Ser Arg Ile
275 280 285

Thr Val Val Ala Val Gln Ala Ser Ser Ala Gln Arg Lys Val Gln Arg
290 295 300

Gly Arg Arg Met Lys Arg Thr Asn Cys Leu Leu Ile Ser Ile Ala Ile
305 310 315 320

Ile Phe Gly Val Ser Trp Leu Pro Leu Asn Phe Phe Asn Leu Tyr Ala
325 330 335

Asp Met Glu Arg Ser Pro Val Thr Gln Ser Met Leu Val Arg Tyr Ala
340 345 350

Ile Cys His Met Ile Gly Met Ser Ser Ala Cys Ser Asn Pro Leu Leu
355 360 365

Tyr Gly Trp Leu Asn Asp Asn Phe Arg Cys Asn Val Gln Ala Ala Ala
370 375 380

Arg Lys Arg Arg Lys Leu Gly Ala Glu Leu Ser Lys Gly Glu Leu Lys
385 390 395 400

Leu Leu Gly Pro Gly Gly Ala Gln Ser Gly Thr Ala Gly Gly Glu Gly
405 410 415

Gly Leu Ala Ala Thr Asp Phe Met Thr Gly His His Glu Gly Gly Leu
420 425 430

Arg Ser Ala Ile Thr Glu Ser Val Ala Leu Thr Asp His Asn Pro Val
435 440 445

Pro Ser Glu Val Thr Lys Leu Met Pro Arg
450 455

<210> 7
<211> 1073
<212> DNA
<213> D. melanogaster


```

<4 15 7
atgg.aaaca caacatggtt ggttaattt aacttaattt caaagaaat tgaagaaat 6
atca ctcat tcttaacaa caaagatgtt ctgcaatca atggcaattt gtcgtgata 12
gtggattctt tcttggtgtt ctgcaatca atggcaattt tggcaatct gtcgtgata 18
ctgggggttg tcttaacaa caacatggtt tggcaatca atggatgat tgcgaattt 24
gttg cgttg atctgatgtt cgttaattt tgcattctct tcaaggcaac cgaattacatg 30
gtgtctact ggcataatgg aaggttcttg tgcagatgtt tcaagtaact gattgtggtg 36
aaggctcttg cctcaatctt cagctgtgtt ctaattgtca tggatcgtt cctggcgttg 42
gttcaatctt tctgtctgtg gatgatggtt aaggagaata tcaactgat tgcatactg 48
actcgtgga tctgtgtgtt ggtgtgttg gtgcagatgtt cctcaatctt caaggtgtg 54
gtggactatg atgcaaaaga gaacatctac taaggcatgt gcaactctac gacgaacgac 60
ttctgtgtt cgcgaacta caaggtctac ttctcaatca gctctactt gctgcccgtg 66
atga:catca ggggtctctt catgctgatg atcatcgggc tctggcgcca gggaaccggc 72
gtcaatctt caaaggatgt gcagcgggtt cgaagcggg tcaaccgact cgtcgtcgtg 78
gtggcatg ccttggtctt gctctgtgtt cctgtcagc tcaactctgt gctcaagtca 84
ctggatgtt tggagaaga caactctac aagctagtca tcaaggtcac cgcacagact 90
ctggctata gacgtctgtt tatcaatctt ctgtctatg cctctctctt cagagaattt 96
cggaaggctt tctataagg cgttaatttg tctctctgtt accagaacta cacatctgat 102
ttgcggcgtt cgcgaagac gctctgtgtt aggaactctt caactggact cta 1073

```

<210 - 8
 <211 - 357
 <212 - PRT
 <213 - D. melanogaster

<400 - 8

Met Glu Asn Thr Thr Met Leu Ala Asn Ile Ser Leu Asn Ala Thr Arg
 1 5 10 15

Asn Glu Glu Asn Ile Thr Ser Phe Phe Thr Asp Glu Glu Trp Leu Ala
 20 25 30

Ile Asn Gly Thr Leu Pro Trp Ile Val Gly Phe Phe Phe Gly Val Ile
 35 40 45

Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val
 50 55 60

Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu
 65 70 75 80

01-0118-NTL6.txt

Ala Ala Ala Asp Leu Met Phe Val Ile Leu Lys Ile Pro Phe Thr Ala
115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130

Thr Asp Tyr Met Val Tyr Tyr Trp Phe Tyr Gly Arg Phe Trp Cys Arg
131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146

Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162

Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile
163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178

Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val
179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194

Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210

His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226

Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242

Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258

Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290

Leu Val Val Val Val Val Ile Ala Phe Ala Ser Leu Trp Leu Pro Val
291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306

Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322

Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338

Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe
339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354

Arg Lys Ala Phe Tyr Lys Ala Val Asn Cys Ser Ser Arg Tyr Gln Asn
355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370

Tyr Thr Ser Asp Leu Phe Phe Irs Arg Lys Thr Ser Lys Ala Arg Thr
341 342 343

Ser Thr Thr Gly Leu
355

<211> 9
<211> 1559
<212> DNA
<213> D. melanogaster

<400> 9
atggagaatc gcagtgactt cgaggcggat gactacggcg acatcagttg gagcaattgg 70
agcaactgga gcaccccccg cggcgccctt ttctgggaca tgagcagcgt gctctcagcc 111
agcaaccata cgcacctgac ggaatttggc caggagctcg cctatccac cagctccttc 150
aatcacagcc agacccctat caccgacacg ccgcgcgtcg gggacgtgga agacggggcc 190
gaggatgggg cggcgctccat ggagacgggc tcgtttgcat ttgtggctcc gtggtggcgt 230
caggtgctct ggagcctcct ctccgggggc atggctcattg tggcgaaggc cggtaacctg 270
attgttgtct ggatcgagat gacgacaaag cggatgggga cggtaaccaa ctatttcata 310
gtgaatctct ccaccgcgga cggcctgggtg tccagcctaa acgtcacctt caactactac 350
tatatgtgtg atagcgactg gcctctgggc gaggctcact gcaagttgtc ccagttcctc 390
ggatgctcaa gcctccgggc ctccagtgctc accctaattg ccctctccat ccacagatac 430
gtggccatca tccggccact gcagccggcg atgagcaagc ggtgcaacct ggccatcgcg 470
ggggctcctc ggctgggctc cagcctcctc tccctgcctc tgatgatcat ctacccgacg 510
gaggaggtgc cggctccggc gctcagcaac cgcacggctc gctaccggga gtggcccgat 550
gggcccacaa atcactccac gatggagctc ctctacaaac tccctcctat cctcctaaac 590
tacttctctc ccctcgtctc cctgacgggc acctactcgc cggctgggct ccagctctcg 630
ggatccaaaga ccctcgggga gtgcacggcc cggcaggttg aaaygtggc gagtaagcga 670
agggctggta agatgatgat tgggtgctgc ctgatattcg ccctctgctg gctgcctctc 710
cacagctact tcataatcac atccctgctac ccggccatca cggaggcgcc ctccatccag 750
gaactctaac tggccatcta ctggctgggc atgagcaact ccctgtacaa tcccattata 790
tactgctgga tgaattcggc ctctcgtctt ggtttcaaga tggctcttcg ctggtgctcg 830
tttctcggcg tgggcactga accttttagt cggcgggaga acctgacatc ccgttactcc 870
tjctccgggtt ccccgcatca caatcgcatc aagcgcaatg ataccagaa atcgatactt 910
tatacctgct ccagctcctc caagtcgcat cgaatttgcg acagcggaac aggtcgcagt 950
ggcagctctc ggaacagctc ggcggcgag tccctgtctc ccggcgcatc tgggtgtgga 990
gggcacagga aacggttgtc ctaccagcag gaaatgcagc agcgttggtc aggaacccat 1030
agtgcacccg cagtgaacaa tccagcagc acggccacaa ccacccaaat gctctctg 1070

<210> 1:
 <211> SIP
 <212> PPT
 <213> D. melanogaster

<400> 1:

Met Glu Asn Ala Ser Asp Phe Ala Ala Asp Asp Tyr Gly Asp Ile Ser
 1 5 10 15

Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val Leu Phe Ser
 20 25 30

Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro Leu Pro Asp
 35 40 45

Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn His Ser Gln
 50 55 60

Thr Leu Ser Thr Asp Gln Pro Ala Val Gly Asp Val Glu Asp Ala Ala
 65 70 75 80

Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala Phe Val Val
 85 90 95

Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly Gly Met Val
 100 105 110

Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile Val Met Thr
 115 120 125

Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ser
 130 135 140

Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe Asn Tyr Tyr
 145 150 155 160

Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr Cys Lys Leu
 165 170 175

Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val Phe Thr Leu
 180 185 190

Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg Pro Leu Gln
 195 200 205

Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala Val Ile Trp
 210 215 220

Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile Tyr Arg Thr
 225 230 235 240

Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val Cys Tyr Pro
 245 250 255 260

Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu Ser Leu Tyr
 265 270 275

Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile Val Ser Met
 275 280 285

Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly Ser Lys Thr
 290 295 300

Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg Ser Lys Arg
 305 310 315 320

Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe Ala Ile Cys
 325 330 335

Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys Tyr Pro Ala
 340 345 350

Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala Ile Tyr Trp
 355 360 365

Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr Cys Trp Met
 370 375 380

Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg Trp Cys Leu
 385 390 395 400

Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu Asn Leu Thr
 405 410 415

Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg Ile Lys Arg
 420 425 430

Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser Ser Pro Lys
 435 440 445

Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala Thr Leu Arg
 450 455 460

Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser Gly Gly Gly
 465 470 475 480

Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln Gln Arg Trp

Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser Val Thr Ala
 508 512 516

Asn Thr Thr Gln Leu Leu Ser
 518

<210> 11
 <211> 1568
 <212> DNA
 <213> D. melanogaster

<400> 11
 atggagaatc gcagtgactt ccaggcggat gaatacggcg acatcagttg gagcaattgg 60
 agcaattgga gcaactgtag caccaccgac ggagtccttt cctcggccat gaggagagtg 120
 ctctcggcca gcaaccatcc gctctcgccg gaatttgccc aggagctcgc cctatccacc 180
 agtcccttca atcacagcca gaacctatcc accgacctgc ccgcgcgtcg ggacgtggaa 240
 gacggggccg aggatcgccc ggagtcctat gagacgggct cgtttgcatt tgtggtcctg 300
 tggtaggggt aggtgctctg gacgctctcc ttggcggcca tggtcattgt ggcgacgggc 360
 ggtaacctga ttgttgcttg gatctgtatg acgaccaaag ggatgcggac ggtaacctaa 420
 tattccatag taaatctctc catcggggac gcatgggtgt ccagcctgaa cgtcacctcc 480
 aactactact acatgctgga tagcgactgg ccttcggcg agttctactg caagttgtcc 540
 cagttccatg cgatgctaa gctctggccc ccaggttcca cctaatggc catctccacc 600
 gacagatacg tggccatcat ccggccactg cagccgggga tgagcaagcg gtgcaacctg 660
 gccatcgagg cggtcctctg gctggcctcc accgctcatc cctgcctcat gatgacatc 720
 taccgcacgg aggaggtgac ggtccgggg ctcagcaacc ggaaggctcg ctaccggag 780
 tggcccgatg ggcccaacca tcaacctaac atggagtcct ctacaacat cctcatcacc 840
 attctaacct acttcctgcc catcgtctcc atgacgggtc cctactcgcg cgtgggcacc 900
 gagctctgg gatccaagac catcggcgag tgcacggccc gccaggtgga gaatgtgcgg 960
 agtaagcgaa gggtagtgaa gatgatgatt gtggctgtcc tgatattcgc catctgctgg 1020
 ctgccttccc acagctactt cataatcaca tctgtctacc cggccatcac ggaggcgccc 1080
 tccatccagg aactttacct ggccatctac tggctggcca tgagcaactc catgtacaat 1140
 cccattatat actgctggat gaattcgcc ttctgtctat gttccaagat ggtcttcgcc 1200
 tggtagctgt ttgtggcgtt gggaactgaa ccttttagtc ggcgggagaa cctgacatcc 1260
 cggtaactct gctccggttc ccgggacac aatgcctca agcgcaatga taccagaaa 1320
 tcgatacttt atacctgtcc cagctcacc aagtcgcacc gaatttcgca cagcggaaac 1380
 ggtgcagtg cgaagctgag gaacagtctc ccggcgaggt cattgtgttc cggtaggact 1440

417.101.3711.txt

ggaggtggag gacacagaa aggtttgtcc tacacagag aaatycapaa goggtugica 150
ggadcaata gggacagag atgacaaat tacacagaa gggcaacac caccacag 155
ctctctctg 156

<211> 12
<211> 522
<212> PRT
<213> D. melanogaster
<400> 12

Met Glu Asn Arg Ser Asp Phe Glu Ala Asp Asp Tyr Gly Asp Ile Ser
1 5 10 15

Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val
20 25 30

Leu Phe Ser Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro
35 40 45

Leu Pro Asp Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn
50 55 60

His Ser Gln Thr Leu Ser Thr Asp Leu Pro Ala Val Gly Asp Val Glu
65 70 75 80

Asp Ala Ala Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala
85 90 95

Phe Val Val Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly
100 105 110

Gly Met Val Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile
115 120 125

Val Met Thr Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val
130 135 140

Asn Leu Ser Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe
145 150 155 160

Asn Tyr Tyr Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr
165 170 175

Cys Lys Leu Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val
180 185 190

Phe Thr Leu Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg
195 200 205

Pro Leu Glu Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala
210 215 220

Val Ile Trp Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile
225 230 235 240

Tyr Arg Thr Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val
245 250 255

Cys Tyr Pro Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu
260 265 270

Ser Leu Tyr Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile
275 280 285

Val Ser Met Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly
290 295 300

Ser Lys Thr Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg
305 310 315 320

Ser Lys Arg Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe
325 330 335

Ala Ile Cys Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys
340 345 350

Tyr Pro Ala Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala
355 360 365

Ile Tyr Trp Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr
370 375 380

Cys Trp Met Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg
385 390 395 400

Trp Cys Leu Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu
405 410 415

Asn Leu Thr Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg
420 425 430

Ile Lys Arg Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser
435 440 445

Ser Pro Lys Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala
450 455 460

*1297123.ST15.txt

Thr Leu Arg Asn Ser Leu Phe Ala Glu Ser Lys Ser Ser Gly Gly Ser
488 489 490 491 492

Gly Gly Gly Gly His Arg Lys Arg Leu Ser Tyr Glu Glu Ala Met Glu
493 494 495 496 497 498 499 500

Glu Arg Trp Ser Gly Phe Asn Ser Ala Thr Ala Val Thr Asn Ser Ser
501 502 503 504 505 506 507 508 509

Ser Thr Ala Asn Thr Thr Glu Leu Leu Ser
510 511 512 513 514 515 516 517

<210> 13
<211> 1394
<212> DNA
<213> D. melanogaster

<400> 13
atggagcacc acaatagcca tctgttgccg ggtggcagcg agaagatgta ctacatagct 60
taccagcagc cgatgctgag gaacgaggat gataactacc aggaggggta cttcatcagg 120
cgggaccccg catccttact ttacaatacc accggaactg cagcggagca tgaagggtcc 180
aactatggat atggctccac cacaacgctc agtggccctc agttcgagac ctataatata 240
actggtatga tgaactttag ctgtgacgac tatgaccttc tatcggagga catgtggtct 300
tgtgcctact ttaagatcat cgtctacatg ctctacatcc ccatctttat ctgcgccctg 360
atcggcaacg gaacgggttg ctatatcgtc tattccacac ctgcgacgag caccggtcac 420
aattacttta tagccagatt ggccatcggc gacatccctg tgcctctctt ctgcgcttcg 480
tcgtccttca tctcgtctgt cctcctgaac tactggcctt ttggcctggc cctctgtcac 540
ctgtgaaact actcgcagcg ggtctcagtt ctggtcagcg ctatacttt ggtggcaatt 600
agpatcgacc gctacatagc cattatgttg ccattaaagg caccgacac aaaaacgctat 660
gcaccttcca tcctcgcggg cgttttggtt atcgcacttg ccacggcact tcccataccc 720
atcgtctctg gactcgacat cccaatgtcg ccgtggcaca cgaaatgaga gaaatacatt 780
tgcgcgaaa tctggccctc ggggaacgag gactactact acaacctgtc cctcttcgag 840
ctgcagttcg tctgcccgtt gggcgctctc atcttcacct agcccgagat caccattcgc 900
gtctggcgga aacgaccgct aggcgagggg gaaaccaacc ggcaccagcg gatggcaccg 960
tccaaacgga agatggctca aatgatgctg acggttgtga ttgtgttcac ctgtgtttgg 1020
ctgccttcca atattttgca gcttttactg aacgacgagg agttcgccca ctgggactct 1080
ctgcgtatg tatggttcgc gtttcactgg ctggcctatg cgcactgttg ctacaatcgc 1140
atcatctact gctacatgaa cgcgcgttcc aggcgaggat tctccagct gatgcaccgt 1200
atgcgccgga tgcgtcgtg gtgctgcctg cggagcgtcg gtgatcgcat gaacgcaatt 1260
tcgggaacgg gtccagcaat tctctcaat cgaatgacaa cctccaccag ctacatcac 1320

0107.103.0115.txt

gctatgtgaa agcagagaga gaaatgttg agagagaaa gattatata agagagagaa: 1874
 toaccactga ggtta 1874

<211> 14
 <211> 184
 <212> PRT
 <213> D. melanogaster

<400> 14

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met
 1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn
 20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
 35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
 50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
 65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
 85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
 100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
 115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
 130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
 145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
 165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
 180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
 195 200 205

0097.10F.0715.txt

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr
260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp
340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
405 410 415

Met Asn Ala Thr Ser Gly Thr Gly Pro Ala Leu Pro Leu Asn Arg Met
420 425 430

Asn Thr Ser Thr Thr Tyr Ile Ser Ala Arg Arg Lys Pro Arg Ala Thr
435 440 445

Ser Leu Arg Ala Asn Pro Leu Ser Cys Gly Glu Thr Ser Pro Leu Arg
450 455 460

<210> 15

<210> 1586
 <212> DNA
 <213> D. melanogaster

<410> 15
 atggagcacc acaatagcga tctgttgcct gctggtagcg agaaatgga ctacatagct 7
 caccagcagc ccatgtctcg gaaagagcat gataactacc aggagggcta ctccatcagc 121
 cgggacccctg cctccttaac ttacaataac aacgcactgc cagaggagca tgaagggtcc 141
 aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatata 161
 actg: gatga tgaacttttag ctgtgaacga catgaacctc tatcggagga catgtggctc 201
 agtgcctact ttaagatcat cgtctacatg ctctacattc ccatctttat ctccgcctcg 241
 atggcacaag gaacggctcg ctatactgtc tattccacac ctgcctagcg cagggtccac 281
 aattacttta tagccagctt ggccatcggc gacatcctga tgcctctctt ctgcgttcgc 321
 cctgtcttca tctcgtcttt cctcctgaac tactggcctt ttggcctggc cctctgtcac 361
 ttctgtgaact actgcagcg ggtctcagtc ctggtcagcg cctatacttt ggtggcaatt 401
 agcattgacc gctacataga cattatgttg ccattaaagc cagccatcac aaaacgctat 441
 gccaccttca tcatcgcccg cgtttcgttt attgcacttg ccacccgaact tcccataccc 481
 atcgtctctg gaactcgacat cccaatgtcg cctgtggcaca cgaatgcga gaaatacatt 521
 tgcgcgcaaa tctggccttc ggggacgcag gactaactac acacccctgc cctcttcgcg 561
 ctgcagttcg tctgtccgct gggcgtgcct atcttcacct acgcccggat caccattcgc 601
 gtcttggcga aacgacccgc aggcgagggg gaaacccaac gcgaccagcg gatggcacgc 641
 tccaaacgga agatggcaca aatgatgtcg acggctgtga tctgttcac ctgcctcttg 681
 ctgccttcca atattttgca gcttttaactg aacgacgagc agttcgccca ctgggatcct 721
 ctgcctgtat tctgtgttcg gtttcacttg ctggccatgt cgcactgctg ctacaatcgc 761
 atcatctact gctacatgaa cgcctgttcc aggagcggat tcttcagct gatgcaccgt 801
 atgcctgggc tgcgtcgtcg gtgcctgcct cggagcgtcg gtgatgcac gaacgcacct 841
 ccgggtgaga tgaactacga gtaccatcgc catgtcggcg atgcctatt ccggaaaccc 881
 aaaatatgca ttaggaacgg gtccagcaat tctctcaat cgaatgaaca catccaccac 921
 ctacatcagc gctcgtcgaa agccacgagc gacatctttg cgagcgaacc cattatcag 961
 cggcgagacg tcaccactgc ggtagctgtc atatcaaaaa ataaaaactga ttcacgggtg 1001
 cgcctgatcg gaagctcagg tggaacagaa gcaaacataa gaagcaccca gttttg 1041
 1586

<210> 16
 <211> 516
 <212> PRT
 <213> D. melanogaster

<410> 16

ELP7.105.ST11.txt

Met Gln His His Asn Ser His Leu Leu Phe Gly Gly Ser Gln Lys Met
1 5 10

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Gln Asp Asp Asn
20 25 30

Tyr Gln Gln Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Gln Gly Ser Asn Tyr Gly Tyr
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Gln Thr Tyr Asn Ile
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Gln
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

Gln Lys Tyr Ile Lys Arg Gln Met Trp Pro Ser Arg Thr Gln Gln Tyr

171

175

177

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
178 181 183

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
184 186 188 191

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
192 194 196 198 201 203 205 207 209

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
210 212 214 216 218 221 223 225 227

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp
228 230 232 234 236 238 241 243 245 247

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
248 250 252 254 256 258 261 263 265 267

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
268 270 272 274 276 278 281 283 285 287

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
288 290 292 294 296 298 301 303 305 307

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
308 310 312 314 316 318 321 323 325 327

Met Asn Ala Thr Ser Gly Glu Met Thr Thr Lys Tyr His Arg His Val
328 330 332 334 336 338 341 343 345 347

Gly Asp Ala Leu Phe Arg Lys Pro Lys Ile Cys Ile Arg Asn Gly Ser
348 350 352 354 356 358 361 363 365 367

Ser Thr Ser Ser Gln Ser Asn Glu His Ile His His Leu His Gln Arg
368 370 372 374 376 378 381 383 385 387

Ser Ser Lys Ala Thr Ser Asp Ile Phe Ala Ser Glu Pro Ile Ile Met
388 390 392 394 396 398 401 403 405 407

Arg Arg Asp Val Thr Thr Ala Val Ala Val Ile Ser Lys Asn Lys Thr
408 410 412 414 416 418 421 423 425 427

Asp Ser Pro Val Arg Arg Ser Gly Ser Ser Gly Gly Thr Glu Ala Asn
428 430 432 434 436 438 441 443 445 447

Ile Arg Ser Thr Glu Phe
448 450

<210> 17
 <211> 1628
 <212> DNA
 <213> D. melanogaster

<400> 17
 atggcaatgg aattaataga gaaggagtaa cgaatggaat tctggccgg agcagaggag 60
 gaagcagaat ttgagcgtct atacggggtt cgcgtgaga ttgtggcct gtgttcatt 120
 ttctatgggg gaatcagtat cgtggccgtc attggcaaca ctttggtcct ctgggtggtg 180
 gccacgacca ggcaaatgcg gaccgtgaca aatatgtata tgcctaattt ggcttttgcg 240
 gatgtgatta ttggcctctt ctgcataaca ttccagttcc aggtgcctct gctgcagagt 300
 tggaaacctgc cgtggttcct ctgcagcttc tgcctcttgc tccaggccct gagtgtaaat 360
 gtctgggtat tcaagctgac cgttcattga atcgatcgga ataggggcct cattaatcca 420
 cttaggggac gtcccaccaa gttcgtatcg aagttcataa ttgggtggaat ttggatgctg 480
 gccctgctat ttgggtgctc ctttggcatt gcccttcgtg tggaggagt ttaccgaaaga 540
 tttcgggaga acaatgagac ctacaattgg acggggcctt tctgcatgaa caagaaccta 600
 tccgatgata aattgcaatc ctttcgctac accctgggtt ttgtgcagta tctggttcca 660
 tctcgtgtca tcaagcttgt ctacatccag atggcggtac gattgtgggg cacacgtgct 720
 cctggttaacg cacaggattc acgggacata acgtgttga aaaacaagaa gaaggtcctc 780
 aaaatgctga ttatcgttgt cattatcttt ggatctgct ggtgcacct gcagctctat 840
 aatattctgt atgtcacgat accggaaatc aacgactacc acctcattag catcgtctgc 900
 tttcgttggg attggctggc catgagcaat agctgctaca acccttttat ttatggcctc 960
 tacaatgaaa aatttaagcg ggaattcaac aagcgatttg cggcctgttt ctgcaagttc 1020
 aagacgggca tggacgcaca cgaaaggacc ttttcgatgc acacccgcgc cagctccata 1080
 aggtcaacct accccaactc ctcgatggga atccggagta atctctttgg tccggcgcgt 1140
 ggtggtgtca acaatgggaa gcggggcttg catatgcgc gggtagcatg atccgtgct 1200
 aacagcggca tttaacaacg aagtagtggg cagaacaaca atgtcaatgg caaacatcat 1260
 cagcatcaaa gctggtttac ctttgcgggc actccgggtg ttccggcacc aggtgttggc 1320
 gttgcaatgc cgcctggcg ggaacaaca ttcgaacctc tgcatacgaa cgtaatcgaa 1380
 tggcagggag aggtggcact catggagctg ccatacaaca cgcctccag cgaggagtgc 1440
 gcatacgggg ccggagtcca gttggccttg ctaagcaggg agagctccag ctgcatttgc 1500
 gaacaggaa ttggcagcca aacccaatgc gatggcact gcatactcag cgaggtgtcg 1560
 cgagtcacac tgcctggctc gcaggcgaag gacaaggatg cgggcaagtc cttgtggcaa 1620
 ccacttta 1628

<210> 15
 <211> 141
 <212> EFT
 <213> 11. Melanogaster

<400> 15

Met Ala Met Asp Leu Ile Glu Gln Glu Ser Arg Leu Glu Phe Leu Pro
 1 5 11 15

Gly Ala Glu Glu Glu Ala Glu Phe Glu Arg Leu Tyr Ala Ala Pro Ala
 20 25 30

Glu Ile Val Ala Leu Leu Ser Ile Phe Tyr Gly Gly Ile Ser Ile Val
 35 40 45

Ala Val Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg
 50 55 60

Gln Met Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala
 65 70 75 80

Asp Val Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala
 85 90 95

Leu Leu Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro
 100 105 110

Phe Val Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala
 115 120 125

Ile Ala Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg
 130 135 140

Pro Thr Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu
 145 150 155 160

Ala Leu Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu
 165 170 175

Leu Thr Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg
 180 185 190

Pro Phe Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe
 195 200 205

Arg Tyr Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile
 210 215 220

Ser Phe Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala
 225 230 235 240

Pro Gly Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys
245 255

Lys Lys Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu
260 265 270

Cys Trp Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro
275 280 285

Glu Ile Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp
290 295 300

Trp Leu Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile
305 310 315 320

Tyr Asn Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys
325 330 335

Phe Cys Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser
340 345 350

Met His Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser
355 360 365

Met Arg Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn
370 375 380

Asn Gly Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala
385 390 395 400

Asn Ser Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Val Asn
405 410 415

Gly Gln His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro
420 425 430

Gly Val Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg
435 440 445

Asn Asn Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp
450 455 460

Val Ala Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu
465 470 475 480

Ala Ser Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser
485 490 495

Ser Cys Ile Cys Glu Glu Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly
500 510 511

Thr Cys Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln
515 520 525

Ala Lys Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu
530 535 540

<210> 19
<211> 1451
<212> DNA
<213> D. melanogaster

<400> 19
atgtttacgt ggctgatgat ggatgtctct cagtttctga aaggggaaat gacagccgat 60
tcagaggcaa atgcacaaaa ttggtataac acgaacgaga gtttatatac caccggaactg 120
aacatagat ggattagtg tagttccaca attcagccag aggagtcctt ttatggcaat 180
gatttgccca cctatcaaca ttgcatagac acgggaatt cttttgtga ctgttccact 240
gtgggtctct acggatttgt gtgcattatc ggattatttg gcaacacctt ggtgatctac 300
gtgggtttgc gcttttccaa aatgcaaaag gtacgaata tatatctct gaatctggcg 360
gtggcagagc agtgcttctt gatttgaata cctttctgc tctacacat gogaatttgc 420
agctgggatc tgggggagtt tatgtgcaaa gctacatgg ttagcacatc catcacctcc 480
tccactctgc agattttctt gctcatcatg tccgggata gatataagc ggtatgccac 540
ccgatttctt cgcacagata cgaactctg catattgca aagtggctct agcgattgac 600
tggtaacctc cagcggctct catgctgccc gtgacctct atgcagcac tgtggagcag 660
gaggatggca tcaattactc gtgcacata atgtggcag atgggtacaa gaagcattcg 720
ggcaccacct tcatactgta cacattttc ctaggattcg ccacaccgt gtgctttatc 780
ctgagttctt actacttggc tataaggaaa ctgcgatgg tgggtcccaa accaggaaag 840
aagtccaaag agaagaggcg ggctcacagg aaggtcactc gactggtaat gacggtgata 900
agtgtatata ttctatgttg gctccctcac tggatttctc agtgggccct gattcactcg 960
aatcccgccg aaagggacct ctcccgactg gaaatactca ttttctact ttggggggca 1020
ctggtttact cgaattcgcc ggtgaatccc atactttatg ctttcttaag tgagaacctc 1080
cggaagagct tcttcaagcc ctttactgtt atgaataagc aggatatcaa cgtccaactc 1140
cagctggagc ccagtgcttt caccaaaacg ggcagtaaaa agaggggtgg ctccaagccg 1200
ctgttgacca gcaatccgca gattcctcaa ctgctgcac tgaatggggg taacaacat 1260
tcctcgacca ccacatcttc gaccacgaca ggggaaaaga ccggaaccac ggggacacag 1320
aaatcatgca attccaatgg caaagtgaca gctccgcccg agaatttgat tatatgttgc 1380

asapagagag asagagagagat agagagagag agagagagag agagagagag agagagagag 144
asagagagag 1481

1210> 20
1211> 40
1212> PRT
1213> D. melanogaster

1400> 20

Met Phe Thr Trp Leu Met Met Asp Val Leu Gln Phe Val Lys Gly Glu
1 5 10 15

Met Thr Ala Asp Ser Glu Ala Asn Ala Thr Asn Trp Tyr Asn Thr Asn
20 25 30

Glu Ser Leu Tyr Thr Thr Glu Leu Asn His Arg Trp Ile Ser Gly Ser
35 40 45

Ser Thr Ile Gln Pro Glu Glu Ser Leu Tyr Gly Thr Asp Leu Pro Thr
50 55 60

Tyr Gln His Cys Ile Ala Thr Arg Asn Ser Phe Ala Asp Leu Phe Thr
65 70 75 80

Val Val Leu Tyr Gly Phe Val Cys Ile Ile Gly Leu Phe Gly Asn Thr
85 90 95

Leu Val Ile Tyr Val Val Leu Arg Phe Ser Lys Met Gln Thr Val Thr
100 105 110

Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile
115 120 125

Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe
130 135 140

Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser
145 150 155 160

Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile
165 170 175

Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile
180 185 190

Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met
195 200 205

Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile

Thr Asp Leu

<211> 21
 <211> 1784
 <212> DNA
 <213> D. melanogaster

<400> 21
 atgttcaact acgaggaggg ggatgcccac caggcggcca tggctgcaga ggtgcctat 80
 agggcaactgc tccactacta tgcacaatgg ccaagtggcg cgggtcacat agtgtcgtc 160
 aacgtggcac cctacaatgg aactggaaac ggaggcaactg tctccttggc gggcaatgag 240
 acaagcaggt atggcgatga tgatagggat ggcctatattg acaccgagcc cagtgaactg 320
 gtcacggaac tggccttctc cctgggtacc agttcaagtc caagtccag ttcacacccc 400
 gcttcacagt ccagtaattc cactgggatg cccgtctggc tgataccag ctatagcgtg 480
 attctgctgt tggcgtgct gggcaactg ctggtcatct ggaagctggt gcagaatgc 560
 cggatgcgtc ccataaccaa cgtgttctctg ctcaacctgg ccatactgga catgtgctg 640
 gggtgctctg gcctgcccgt caccctgggtg ggcacccctg tgcgaaaact catctttggc 720
 gagttcctct gcaagccttc tcaattctcg caagccgctt cgtggtccgt ttctgctgtg 800
 accctgggtg ccatactctg tgagcgctac tacgcgatat gccatccact ggcctcggga 880
 tcttggcaga caatcagtc cgcctacaag atcatcggtt tcatctgggt gggcggcctc 960
 ctctgcctga cgcctcagtc ggcctctagt caactgatac ccaccagtcg accgggtcac 1040
 tgcgaagtgc gtgagttttg ggcgcacacg ggatacagag tctctacaa catctgctg 1120
 gactctctgc tgcctgctct ggcgtctctc gtctctctgc tggcctacat cctcatcag 1200
 cgtacccctg acgtaggcat ggccaaggac agcggagcca tctgcagca atcgtgctt 1280
 gtttcctgta caacggccgg cgggaagcga ccgaatccgg gcaccagcag cagttagtaac 1360
 tgcacccctg tctgcacgc caccgcagtc tataatgaaa atagtaacaa taataatgga 1440
 aattcagagg gatccgagc cggaggatca accaatatgg caacgaccac cttgacaaag 1520
 agaccaacgg ctccaactgt gatcaccacc accacgacga ccacggtgac gctggccaag 1600
 accctctcgc ccagcattcg cgtccaggat ggggcacttc gcaggtccaa ctagggccaag 1680
 accctggaga gcaagaagcg tgtggccaag atgtctctcg tctggtgct ggagttcttc 1760
 atctgctgga ctccgctgta cgtgatcaac acgtatggtc tctgcatcg accggtggtg 1840
 tacgagtatg tgactacac gccatcagt tctctcagc tctggtccta ctcatccag 1920
 tctgcaatc cgatcaccta ctgttctatg aaagccagct tccgggcgcg ctttgtcgac 2000
 accctcaagg gtctgcctg gcgtctgga gcaggtgcca gggaggcgt cgggtggtgt 2080
 gctggtggag gactctcgc cagcaggcg ggcgcaggcc cgggcgcta tgcagtgac 2160

aaacacaaacaa ttatgtctcaaa tcccttgcata gcatatggta tggacacatg tggatctatg 166
 tcaagccaaag agttttctcaa tgggttgggtg accacacata gtcgagcagc agtcgtcaaa 174
 agttctcagc tata 1784

<210> 22
 <211> 584
 <212> PRT
 <213> D. melanogaster

<400> 22

Met Phe Asn Tyr Glu Glu Gly Asp Ala Asp Gln Ala Ala Met Ala Ala
 1 5 10 15

Ala Ala Ala Tyr Arg Ala Leu Leu Asp Tyr Tyr Ala Asn Ala Pro Ser
 20 25 30

Ala Ala Gly His Ile Val Ser Leu Asn Val Ala Pro Tyr Asn Gly Thr
 35 40 45

Gly Asn Gly Gly Thr Val Ser Leu Ala Gly Asn Ala Thr Ser Ser Tyr
 50 55 60

Gly Asp Asp Asp Arg Asp Gly Tyr Met Asp Thr Glu Pro Ser Asp Leu
 65 70 75 80

Val Thr Glu Leu Ala Phe Ser Leu Gly Thr Ser Ser Ser Pro Ser Pro
 85 90 95

Ser Ser Thr Pro Ala Ser Ser Ser Ser Thr Ser Thr Gly Met Pro Val
 100 105 110

Trp Leu Ile Pro Ser Tyr Ser Met Ile Leu Leu Phe Ala Val Leu Gly
 115 120 125

Asn Leu Leu Val Ile Ser Thr Leu Val Gln Asn Arg Arg Met Arg Thr
 130 135 140

Ile Thr Asn Val Phe Leu Leu Asn Leu Ala Ile Ser Asp Met Leu Leu
 145 150 155 160

Gly Val Leu Cys Met Pro Val Thr Leu Val Gly Thr Leu Leu Arg Asn
 165 170 175

Phe Ile Phe Gly Glu Phe Leu Cys Lys Leu Phe Gln Phe Ser Gln Ala
 180 185 190

Ala Ser Val Ala Val Ser Ser Trp Thr Leu Val Ala Ile Ser Cys Glu
 195 200 205

Arg Tyr Tyr Ala Ile Cys His Pro Leu Arg Ser Arg Ser Trp Gln Thr
210 215 220

Ile Ser His Ala Tyr Lys Ile Ile Gly Phe Ile Trp Leu Gly Gly Ile
225 230 235 240

Leu Cys Met Thr Pro Ile Ala Val Phe Ser Gln Leu Ile Pro Thr Ser
245 250 255

Arg Pro Gly Tyr Cys Lys Cys Arg Glu Phe Trp Pro Asp Gln Gly Tyr
260 265 270

Glu Leu Phe Tyr Asn Ile Leu Leu Asp Phe Leu Leu Leu Val Leu Pro
275 280 285

Leu Leu Val Leu Cys Val Ala Tyr Ile Leu Ile Thr Arg Thr Leu Tyr
290 295 300

Val Gly Met Ala Lys Asp Ser Gly Arg Ile Leu Gln Gln Ser Leu Pro
305 310 315 320

Val Ser Ala Thr Thr Ala Gly Gly Ser Ala Pro Asn Pro Gly Thr Ser
325 330 335

Ser Ser Ser Asn Cys Ile Leu Val Leu Thr Ala Thr Ala Val Tyr Asn
340 345 350

Glu Asn Ser Asn Asn Asn Asn Gly Asn Ser Glu Gly Ser Ala Gly Gly
355 360 365

Gly Ser Thr Asn Met Ala Thr Thr Thr Leu Thr Thr Arg Pro Thr Ala
370 375 380

Pro Thr Val Ile Thr Thr Thr Thr Thr Thr Val Thr Leu Ala Lys
385 390 395 400

Thr Ser Ser Pro Ser Ile Arg Val His Asp Ala Ala Leu Arg Arg Ser
405 410 415

Asn Glu Ala Lys Thr Leu Glu Ser Lys Lys Arg Val Val Lys Met Leu
420 425 430

Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr Pro Leu Tyr Val
435 440 445

Ile Asn Thr Met Val Met Leu Ile Gly Pro Val Val Tyr Glu Tyr Val
450 455 460

Asp Tyr Thr Ala Ile Ser Phe Leu Gln Leu Leu Ala Tyr Ser Ser Ser
465 470 475 480

Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala Ser Phe Arg Arg
485 490 495

Ala Phe Val Asp Thr Phe Lys Gly Leu Pro Trp Arg Arg Gly Ala Gly
500 505 510

Ala Ser Gly Gly Val Gly Gly Ala Ala Gly Gly Gly Leu Ser Ala Ser
515 520 525

Gln Ala Gly Ala Gly Pro Gly Ala Tyr Ala Ser Ala Asn Thr Asn Ile
530 535 540

Ser Leu Asn Pro Gly Leu Ala Met Gly Met Gly Thr Trp Arg Ser Arg
545 550 555 560

Ser Arg His Glu Phe Leu Asn Ala Val Val Thr Thr Asn Ser Ala Ala
565 570 575

Ala Ala Val Asn Ser Pro Gln Leu
580

0010: 23
0011: 1452
0012: DNA
0013: D. melanogaster

0400: 23
 agtgacgact ccttgatgga cgttggccag acgttggcag ccaggctggc ggatagcgac 60
 ggcaacgggg caaatgacag cggactcctg gcaaccggac aaggctctgga gcaggagcag 120
 gaggtcttgg cactggatat gggcacaat gccagcgcg acggcggaat agtacggtat 180
 gtgcgcgtgc tggacgccc ggagacgtac attgtacccg tctgtacac gtcacatctc 240
 atgtgtggag ttttgggcaa cggcaacgtg gtcacatct tttttggca ccgctccatg 300
 cgcacatag caaacacata cattctttca ctggcctgg ctgatctgtt gggttatattg 360
 gtgtgtgtac ctgtggccac gattgtctac acgcaggaaa gctggccctt tgagcggaac 420
 atgtgcgcga tcagcgagtt ctttaaggac atatccatcg ggtgtccgt gtttacactg 480
 acgcgccttt ccggcgagcg gtactgcgac attgtaaac cctacgcaa gttcagacc 540
 aagcgctca ctgtctttac tgcggtgatg atctggatcc tggccatct actgggcattg 600
 ccttcggttc tttctctcga catcaagtc taccctgtgt tcacagccac cggtaacatg 660
 accattgaag tgtgtctccc atttcgcgac ccggagtatg caaagttcat ggtggcgggc 720
 aaggcaactg tgtaactact gttgcgcgtg tccatcattg gggcgctata catcatgatg 780

gccaaaggcc tccatattgag cgcgcgcaac atgbcgggg aacagcagag catgcagagc 640
 cgcacccagg ctaggggccc actccatgtg gcgcgcattg tggtagcatt cgtgggtggtg 680
 ttcttcatct gcttcttccc gtaccacgtg tttagactgt ggtaccactt ctaccacaacg 960
 gctgaggagg acttcgatga gttctggaac gtgcgcgca tcttctctaa actcgtgcgt 1020
 caaccccggtg gctctactg cgtgtccggg gtgtttcggc agcactttaa tgcctacctc 1080
 tgtgtcatct ggtcaagcg gcagcgcac ctgcggcagc actcaacggc cactggaatg 1140
 atggacaata cagtggtgat gtccatgcgc cgtctcaggt acgtgggtgg aacgctggc 1200
 aatctggggg cctcgtgcga ccggaacagc aatcacggag ttggtggagc tggaggtgga 1260
 ctaggaggag gactaggggc agtctgtgtg ggcagcttct atcggcagga ctgatgcc 1320
 ctgcagcagc gaaatgccc cggaggtggt gcgggcgggg gactctccgg acttgagacc 1380
 gggggcgga cggcggcagt gacgaaaag agctttataa atcgttacga aagtggcgta 1440
 atgcctact aa 1452

#210: 24
 #211: 483
 #212: PRT
 #213: D. melanogaster

#400: 24

Met Tyr Ala Ser Leu Met Asp Val Gly Gln Thr Leu Ala Ala Arg Leu
 1 5 10 15

Ala Asp Ser Asp Gly Asn Gly Ala Asn Asp Ser Gly Leu Leu Ala Thr
 20 25 30

Gly Gln Gly Leu Glu Gln Glu Gln Gly Leu Ala Leu Asp Met Gly
 35 40 45

His Asn Ala Ser Ala Asp Gly Gly Ile Val Pro Tyr Val Pro Val Leu
 50 55 60

Asp Arg Pro Glu Thr Tyr Ile Val Thr Val Leu Tyr Thr Leu Ile Phe
 65 70 75 80

Ile Val Gly Val Leu Gly Asn Gly Thr Leu Val Ile Ile Phe Phe Arg
 85 90 95

His Arg Ser Met Arg Asn Ile Pro Asn Thr Tyr Ile Leu Ser Leu Ala
 100 105 110

Leu Ala Asp Leu Leu Val Ile Leu Val Cys Val Pro Val Ala Thr Ile
 115 120 125

Val Tyr Thr Gln Glu Ser Trp Pro Phe Glu Arg Asn Met Cys Arg Ile

137

147

14

Ser Glu Phe Phe Lys Asp Ile Ser Ile Gly Val Ser Val Phe Thr Leu
148 150 155 160

Thr Ala Leu Ser Gly Glu Arg Tyr Cys Ala Ile Val Asn Pro Leu Arg
165 170 175

Lys Leu Glu Thr Lys Pro Leu Thr Val Phe Thr Ala Val Met Ile Trp
180 185 190

Ile Leu Ala Ile Leu Leu Gly Met Pro Ser Val Leu Phe Ser Asp Ile
195 200 205

Lys Ser Tyr Pro Val Phe Thr Ala Thr Gly Asn Met Thr Ile Glu Val
210 215 220

Cys Ser Pro Phe Arg Asp Pro Glu Tyr Ala Lys Phe Met Val Ala Gly
225 230 235 240

Lys Ala Leu Val Tyr Tyr Leu Leu Pro Leu Ser Ile Ile Gly Ala Leu
245 250 255

Tyr Ile Met Met Ala Lys Arg Leu His Met Ser Ala Arg Asn Met Pro
260 265 270

Gly Glu Glu Glu Ser Met Glu Ser Arg Thr Glu Ala Arg Ala Arg Leu
275 280 285

His Val Ala Arg Met Val Val Ala Phe Val Val Val Phe Phe Ile Cys
290 295 300

Phe Phe Pro Tyr His Val Phe Glu Leu Trp Tyr His Phe Tyr Pro Thr
305 310 315 320

Ala Glu Glu Asp Phe Asp Glu Phe Trp Asn Val Leu Arg Ile Leu Pro
325 330 335

Lys Leu Val Arg Glu Pro Arg Gly Leu Tyr Cys Val Ser Gly Val Phe
340 345 350

Arg Glu His Phe Asn Arg Tyr Leu Cys Cys Ile Cys Val Lys Arg Glu
355 360 365

Pro His Leu Arg Glu His Ser Thr Ala Thr Gly Met Met Asp Asn Thr
370 375 380

Ser Val Met Ser Met Arg Arg Ser Thr Tyr Val Gly Gly Thr Ala Gly
385 390 395 400

Asn Leu Arg Ala Ser Leu His Arg Asn Ser Asn His Gly Val Gly Gly
415 416

Ala Gly Gly Gly Val Gly Gly Gly Val Gly Ser Gly Arg Val Gly Val
420 425 430

Phe His Arg Gln Asp Ser Met Pro Leu Gln His Gly Asn Ala His Gly
435 440 445

Gly Gly Ala Gly Gly Gly Ser Ser Gly Leu Gly Ala Gly Gly Arg Thr
450 455 460

Ala Ala Val Ser Glu Lys Ser Phe Ile Asn Arg Tyr Glu Ser Gly Val
465 470 475 480

Met Arg Tyr

02100 25
02110 10
02120 PRT
02130 Artificial Sequence

02100
02130 Novel Sequence

04000 15

Thr Asp Val Asp His Val Phe Leu Arg Phe
5 10

02100 26
02110 9
02120 PRT
02130 Artificial Sequence

02100
02130 Novel Sequence

04000 26

Asp Pro Lys Gln Asp Phe Met Arg Phe
5

02100 27
02110 7
02120 PRT
02130 Artificial Sequence

02100
02130 Novel Sequence

04000 27

Pro Asp Asn Phe Met Arg Phe

1 5

<210> 15
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> Novel Sequence

<400> 18

Thr Pro Ala Glu Asp Phe Met Arg Phe
 1 5

<210> 19
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> Novel Sequence

<400> 29

Ser Leu Lys Gln Asp Phe Met His Phe
 1 5

<210> 30
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> Novel Sequence

<400> 30

Ser Val Lys Gln Asp Phe Met His Phe
 1 5

<210> 31
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> Novel Sequence

<400> 31

Ala Ala Met Asp Arg Tyr
 1 5

<210> 32
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

6223> Novel Sequence

6401> 32

Jer Val Gln Asp Asn Phe Met His Phe
1 5

6211> 32

6211> 11

6212> FFT

6213> Artificial Sequence

6224>

6224> Novel Sequence

6402> 11

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe
1 5 10

6214> 34

6214> 10

6215> FFT

6216> Artificial Sequence

6225>

6225> Novel Sequence

6403> 34

Gly Asp Gly Arg Leu Tyr Ala Phe Gly Leu
1 5 10

6217> 39

6217> 8

6218> FFT

6219> Artificial Sequence

6226>

6226> Novel Sequence

6404> 31

Asp Arg Leu Tyr Ser Phe Gly Leu
1 5

6210> 36

6210> 18

6212> FFT

6213> Artificial Sequence

6227>

6227> Novel Sequence

6405> 36

Ala Pro Ser Gly Ala Gln Arg Leu Tyr Gly Phe Gly Leu
1 5 10

6210> 37

<211> 9
 <212> PRT
 <213> Artificial Sequence
 <221>
 <223> Novel Sequence
 <411> 37
 Gly Gly Ser Leu Tyr Ser Phe Gly Leu
 1 5

<211> 38
 <212> 4
 <213> PRT
 <213> Artificial Sequence
 <221>
 <223> Novel Sequence
 <411> 38

Phe Ile Arg Phe
 1

<211> 39
 <212> 1
 <213> PRT
 <213> Artificial Sequence
 <221>
 <223> Novel Sequence
 <411> 39

Gly Asn Glu Phe Ile Arg Phe
 1 5

<211> 40
 <212> 4
 <213> PRT
 <213> Artificial Sequence
 <221>
 <223> Novel Sequence
 <411> 40

Phe Met Arg Phe
 1

<211> 41
 <212> 7
 <213> PRT
 <213> Artificial Sequence
 <221>
 <223> Novel Sequence
 <411> 41

Lys Ser Ala Phe Met Arg Phe
1 5

Q210> 42
Q211> 7
Q212> PPT
Q213> Artificial Sequence

Q220>
Q223> Novel Sequence

Q400> 41

Lys Pro Asn Phe Leu Arg Phe
1 5

Q210> 41
Q211> 4
Q212> PPT
Q213> Artificial Sequence

Q220>
Q223> Novel Sequence

Q400> 43

Phe Leu Arg Phe
1

Q210> 44
Q211> 4
Q212> PPT
Q213> Artificial Sequence

Q220>
Q223> Novel Sequence

Q400> 44

Tyr Leu Arg Phe
1

Q210> 45
Q211> 7
Q212> PPT
Q213> Artificial Sequence

Q220>
Q223> Novel Sequence

Q400> 45

Lys Pro Asn Phe Leu Arg Tyr
1 5

Q210> 46
Q211> 8
Q212> PPT
Q213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 46

Thr Asn Arg Asn Phe Leu Arg Phe
 1 5

<210> 47

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 47

Arg Asn Lys Phe Glu Phe Ile Arg Phe
 1 5

<210> 48

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 48

Ala Gly Pro Arg Phe Ile Arg Phe
 1 5

<210> 49

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 49

Gly Leu Gly Pro Arg Pro Leu Arg Phe
 1 5

<210> 50

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 50

Ile Leu
 1

02100 51
02110 8
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 51

Ala Gly Ala Lys Ile Phe Arg Phe
1 5

02100 51
02110 9
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 51

Ala Pro Lys Pro Lys Phe Ile Arg Phe
1 5

02100 53
02110 8
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 53

Lys Ser Ala Phe Val Leu Arg Phe
1 5

02100 54
02110 9
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 54

Thr Lys Phe Gln Asp Phe Leu Arg Phe
1 5

02100 55
02110 10
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 55

Ser Ala Glu Pro Phe Gly Thr Met Arg Phe
1 5 10

6210 56
6211 12
6212 PRT
6213 Artificial Sequence

6220
6223 Novel Sequence

6400 56

Ala Ser Glu Asp Ala Leu Phe Gly Thr Met Arg Phe
1 5 10

6210 57
6211 13
6212 PRT
6213 Artificial Sequence

6220
6223 Novel Sequence

6400 57

Ser Ala Asp Asp Ser Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

6210 58
6211 14
6212 PRT
6213 Artificial Sequence

6220
6223 Novel Sequence

6400 58

Glu Asp Gly Asn Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

6210 59
6211 8
6212 PRT
6213 Artificial Sequence

6220
6223 Novel Sequence

6400 59

Phe Leu Phe Gln Pro Gln Arg Phe
1 5

6210 60
6211 9
6212 PRT
6213 Artificial Sequence

42200

42230 Novel Sequence

44000 60

Ser Ala Asp Pro Asn Phe Leu Arg Phe

1 5

42100 61

42110 4

42120 PFT

42130 Artificial Sequence

42200

42230 Novel Sequence

44000 61

Ser Gln Pro Asn Phe Leu Arg Phe

1 5

42100 62

42110 10

42120 PFT

42130 Artificial Sequence

42200

42230 Novel Sequence

44000 62

Ala Ser Gly Asp Pro Asn Phe Leu Arg Phe

1 5 10

42100 63

42110 8

42120 PFT

42130 Artificial Sequence

42200

42230 Novel Sequence

44000 63

Ser Asp Pro Asn Phe Leu Arg Phe

1 5

42100 64

42110 10

42120 PFT

42130 Artificial Sequence

42200

42230 Novel Sequence

44000 64

Ala Ala Ala Asp Pro Asn Phe Leu Arg Phe

1 5 10

02100 65
 02110 6
 02120 PRT
 02130 Artificial Sequence

02200
 02230 Novel Sequence

04000 65

Pro Asn Phe Leu Arg Phe
 1 5

02100 66
 02110 6
 02120 PRT
 02130 Artificial Sequence

02200
 02230 Novel Sequence

04000 66

Lys Pro Phe Leu Arg Phe
 1 5

02100 67
 02110 10
 02120 PRT
 02130 Artificial Sequence

02200
 02230 Novel Sequence

04000 67

Ala Gly Ser Asp Pro Asn Phe Leu Arg Phe
 1 5 10

02100 68
 02110 7
 02120 PRT
 02130 Artificial Sequence

02200
 02230 Novel Sequence

04000 68

Lys Pro Asn Phe Leu Arg Tyr
 1 5

02100 69
 02110 8
 02120 PRT
 02130 Artificial Sequence

02200
 02230 Novel Sequence

+4000 69

Ser Pro Arg Glu Pro Ile Arg Phe
1 5

+2100 70

+2110 8

+2120 PRT

+2130 Artificial Sequence

+2200

+2230 Novel Sequence

+4000 70

Leu Arg Gly Glu Pro Ile Arg Phe
1 5

+2100 71

+2110 9

+2120 PRT

+2130 Artificial Sequence

+2200

+2230 Novel Sequence

+4000 71

Ser Pro Leu Gly Thr Met Arg Phe
1 5

+2100 72

+2110 11

+2120 PRT

+2130 Artificial Sequence

+2200

+2230 Novel Sequence

+4000 72

Glu Ala Glu Glu Pro Leu Gly Thr Met Arg Phe
1 5 10

+2100 73

+2110 12

+2120 PRT

+2130 Artificial Sequence

+2200

+2230 Novel Sequence

+4000 73

Ala Ser Glu Asp Ala Leu Phe Gly Thr Met Arg Phe
1 5 10

+2100 74

+2110 13

+2120 PRT

218 Artificial Sequence

220

223 Novel Sequence

400 74

Glu Asp Gly Asn Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

210 75

211 10

212 PRT

213 Artificial Sequence

220

223 Novel Sequence

400 75

Ser Ala Glu Pro Phe Gly Thr Met Arg Phe
1 5 10

210 76

211 10

212 PRT

213 Artificial Sequence

220

223 Novel Sequence

400 76

Ser Ala Asp Asp Ser Ala Pro Phe Gly Thr Met Arg Phe
1 5 10

210 77

211 7

212 PRT

213 Artificial Sequence

220

223 Novel Sequence

400 77

Lys Pro Thr Phe Ile Arg Phe
1 5

210 78

211 8

212 PRT

213 Artificial Sequence

220

223 Novel Sequence

400 78

Ala Ser Pro Ser Phe Ile Arg Phe
1 5

0210 79
 0211 7
 0212 PPT
 0213 Artificial Sequence

0220
 0221 Novel Sequence

0400 77

Gly Ala Lys Phe Ile Arg Phe
 1 5

0210 81
 0211 8
 0212 PPT
 0213 Artificial Sequence

0220
 0221 Novel Sequence

0400 8

Ala Gly Ala Lys Phe Ile Arg Phe
 1 5

0210 81
 0211 9
 0212 PPT
 0213 Artificial Sequence

0220
 0221 Novel Sequence

0400 81

Ala Pro Lys Pro Lys Phe Ile Arg Phe
 1 5

0210 81
 0211 7
 0212 PPT
 0213 Artificial Sequence

0220
 0221 Novel Sequence

0400 82

Lys Ser Ala Tyr Met Arg Phe
 1 5

0210 82
 0211 11
 0212 PPT
 0213 Artificial Sequence

0220
 0221 Novel Sequence

4400 83

Ser Pro Met Gln Arg Ser Ser Met Val Arg Phe
1 5 10

4210 84

4211 11

4212 PPT

4213 Artificial Sequence

4220

4223 Novel Sequence

4410 84

Ser Pro Met Glu Arg Ser Ala Met Val Arg Phe
1 5 10

4210 85

4211 11

4212 PPT

4213 Artificial Sequence

4220

4223 Novel Sequence

4400 85

Ser Pro Met Asp Arg Ser Lys Met Val Arg Phe
1 5 10

4210 86

4211 7

4212 PPT

4213 Artificial Sequence

4220

4223 Novel Sequence

4400 86

Lys Asn Glu Phe Ile Arg Phe
1 5

4210 87

4211 7

4212 PPT

4213 Artificial Sequence

4220

4223 Novel Sequence

4400 87

Lys Pro Ser Phe Val Arg Phe
1 5

4210 88

4211 11

<212> PPT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 88

31n Iro Lys Ala Arg Ser Gly Tyr Ile Arg Phe
 1 5 10

<210> 89
 <211> 9
 <212> PPT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 89

Ala Met Arg Asn Ala Leu Val Arg Phe
 1 5

<210> 91
 <211> 12
 <212> PPT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 90

Ala Ser Gly Gly Met Arg Asn Ala Leu Val Arg Phe
 1 5 10

<210> 91
 <211> 10
 <212> PPT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 91

Asn Gly Ala Pro Gln Pro Phe Val Arg Phe
 1 5 10

<210> 92
 <211> 9
 <212> PPT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 92

Arg Asn Lys Phe Gln Phe Ile Arg Phe

1

E

<210> 93
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 93

Ser Asp Arg Pro Thr Arg Ala Met Asp Ser Pro Ile Arg Phe
 1 5 10

<210> 94
 <211> 1
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 94

Ala Ala Asp Gly Ala Pro Leu Ile Arg Phe
 1 5 10

<210> 95
 <211> 1
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 95

Ala Pro Glu Ala Ser Pro Phe Ile Arg Phe
 1 5 10

<210> 96
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 96

Ala Ser Pro Ser Ala Pro Leu Ile Arg Phe
 1 5 10

<210> 97
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 97

Ser Pro Ser Ala Val Pro Leu Ile Arg Phe
1 5 10

<210> 98

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 98

Ala Ser Ser Ala Pro Leu Ile Arg Phe
1 5

<210> 99

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 99

Lys His Glu Tyr Leu Arg Phe
1 5

<210> 100

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 100

Ser Leu Asp Tyr Arg Phe
1 5

<210> 101

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 101

Glu Ile Val Phe His Gln Ile Ser Pro Ile Phe Phe Arg Phe
1 5 10

<210> 102

02110 9
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 112

Gly Gly Pro Ala Gly Pro Leu Arg Phe
1 5

02100 103
02110 8
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 103

Gly Pro Ser Gly Pro Leu Arg Phe
1 5

02100 104
02110 7
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 104

Ala Gln Thr Phe Val Arg Phe
1 5

02100 105
02110 7
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 115

Gly Gln Thr Phe Val Arg Phe
1 5

02100 116
02110 7
02120 PPT
02130 Artificial Sequence

02200
02230 Novel Sequence

04000 116

Lys Ser Ala Phe Val Arg Phe
1 5

62107 107
62111 7
62112 PRT
62113 Artificial Sequence

6220
6223 Novel Sequence

6400 107

Lys Ser Gln Tyr Ile Arg Phe
1 5

62108 108
62111 8
62112 PRT
62113 Artificial Sequence

6220
6223 Novel Sequence

6400 108

Asp Val Pro Gly Val Leu Arg Phe
1 5

62109 109
62111 9
62112 PRT
62113 Artificial Sequence

6220
6223 Novel Sequence

6400 109

Lys Ser Val Pro Gly Val Leu Arg Phe
1 5

62110 110
62111 9
62112 PRT
62113 Artificial Sequence

6220
6223 Novel Sequence

6400 110

Ser Glu Val Pro Gly Val Leu Arg Phe
1 5

62110 111
62111 8
62112 PRT
62113 Artificial Sequence

<223>

<223> Novel Sequence

<400> 111

Ser Val Pro Gly Val Leu Arg Phe
1 5

<210> 112

<211> 12

<212> PRT

<213> Artificial Sequence

<22>

<223> Novel Sequence

<400> 112

Asp Phe Asp Gly Ala Met Pro Gly Val Leu Arg Phe
1 5 10

<210> 113

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 113

Glu Ile Pro Gly Val Leu Arg Phe
1 5

<210> 114

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 114

Trp Ala Asn Gln Val Arg Phe
1 5

<210> 115

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 115

Ala Ser Trp Ala Ser Ser Val Arg Phe
1 5

*2108 116
 *2110 8
 *2112 PPT
 *2113 Artificial Sequence

*2200
 *2210 Novel Sequence

*4000 116

Ala Met Met Arg Phe
 1 5

*2111 117
 *2113 9
 *2115 PPT
 *2116 Artificial Sequence

*2200
 *2210 Novel Sequence

*4000 117

Gly Leu Gly Pro Arg Pro Leu Arg Phe
 1 5

*2117 118
 *2119 9
 *2121 PPT
 *2122 Artificial Sequence

*2200
 *2210 Novel Sequence

*4000 118

Ser Pro Ser Ala Lys Trp Met Arg Phe
 1 5

*2123 119
 *2125 9
 *2127 PPT
 *2128 Artificial Sequence

*2200
 *2210 Novel Sequence

*4000 119

Thr Lys Phe Gln Asp Phe Leu Arg Phe
 1 5

*2129 120
 *2131 10
 *2133 PPT
 *2134 Artificial Sequence

*2200
 *2210 Novel Sequence

*4000 120

Glu Asp Arg Asp Tyr Arg Pro Leu Gln Phe
1 5 10

<210> 121
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 121

Phe Ile Arg Phe
1

<210> 122
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 122

Ala Val Pro Gly Val Leu Arg Phe
1 5

<210> 123
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 123

Gly Asp Val Pro Gly Val Leu Arg Phe
1 5

<210> 124
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 124

Ser Asp Ile Gly Ile Ser Glu Pro Asn Phe Leu Arg Phe
1 5 10

<210> 125
<211> 9
<212> PRT
<213> Artificial Sequence

1492 125

Deriving from the *Journal of the American Medical Association*

•

(210) 126

[illegible]

— 20 —

(212) Artificial Sequence

222

223: Novel Sequence

400 126

Ala Glu Gly Leu Ser Ser Pro Leu Ile Arg Phe

10

210 127

211: 8

0110. PR

0013 Artificial Sequence

150

Novel Sequence

1400 127

Phe Asp Arg Asp Phe Met Arg Phe

1 5

128

221: 8

5220 PFE

3.2.3 Artificial Sequence

1. *Journal of the American Medical Association*, 1997; 277: 1033-1038.

Novel Sequence

400 128

Ala Gly Pro Arg Phe Ile Arg Phe

5

119

88

5.12. P.E.

4.3.3 Artificial Sequence

1. *Journal of the American Medical Association*, 1997; 277: 1033-1037.

4.2.3 Novel Sequence

2400 · 1.29

Gly Met Pro Gly Val Leu Arg Phe

100

<210> 130
 <211> 2
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 130

Ile Leu
 1

<210> 131
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 131

Leu Gln Pro Asn Phe Leu Arg Phe
 1 5

<210> 132
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 132

Gly Pro Asn Phe Ile Arg Phe
 1 5

<210> 133
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 133

Phe Met Arg Phe
 1

<210> 134
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 134

Phe Leu Arg Phe

1

<210> 135

<211> 4

<212> PFT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 135

Tyr Ile Arg Phe

1

<210> 136

<211> 7

<212> PFT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 136

Gly Asn Ser Phe Leu Arg Phe

1

5

<210> 137

<211> 7

<212> PFT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 137

Asp Pro Ser Phe Leu Arg Phe

1

5

<210> 138

<211> 6

<212> PFT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 138

Gln Asp Phe Met Arg Phe

1

5

<210> 139

<211> 9

<212> PFT

0213> Artificial Sequence

0220>

0223> Novel Sequence

0400> 139

Lys Pro Asn Gln Asp Phe Met Arg Phe
1 5

0210> 140

0211> 1

0212> PPT

0213> Artificial Sequence

0220>

0223> Novel Sequence

0400> 140

Thr Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

0210> 141

0211> 6

0212> PPT

0213> Artificial Sequence

0220>

0223> Novel Sequence

0400> 141

Ala Ala Met Asp Arg Tyr
1 5

0210> 142

0211> 9

0212> PPT

0213> Artificial Sequence

0220>

0223> Novel Sequence

0400> 142

Ser Pro Lys Gln Asp Phe Met Arg Phe
1 5

0210> 143

0211> 7

0212> PPT

0213> Artificial Sequence

0220>

0223> Novel Sequence

0400> 143

Pro Asp Asn Phe Met Arg Phe
1 5

<210> 144
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 144

Asp Pro Lys Gln Asp Phe Met Arg Phe
 1 5

<210> 145
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 145

Thr Pro Ala Glu Asp Phe Met Arg Phe
 1 5

<210> 146
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 146

Ser Asp Asn Phe Met Arg Phe
 1 5

<210> 147
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 147

Tyr Leu Arg Phe
 1

<210> 148
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

410> 148

Asp Arg Asn Phe Leu Arg Phe
1 5

4110> 149

4111> 8

4112> PPT

4113> Artificial Sequence

4120>

4123> Novel Sequence

440> 149

Asn Arg Asn Phe Leu Arg Phe
1 5

4110> 150

4111> 10

4112> PPT

4113> Artificial Sequence

4120>

4123> Novel Sequence

4400> 150

Phe Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

4110> 151

4111> 10

4112> PPT

4113> Artificial Sequence

4120>

4123> Novel Sequence

4400> 151

Gln Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

4110> 152

4111> 8

4112> PPT

4113> Artificial Sequence

4120>

4123> Novel Sequence

4400> 152

Phe Leu Phe Gln Pro Gln Arg Phe
1 5

4110> 153

4111> 10

0210 PPT
0213 Artificial Sequence

0220
0223 Novel Sequence

0400 153

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe
1 5 10

0210 154
0211 9
0212 PPT
0213 Artificial Sequence

0220
0223 Novel Sequence

0400 154

Phe Asp Asp Tyr Gly His Leu Arg Phe
1 5

0210 155
0211 9
0212 PPT
0213 Artificial Sequence

0220
0223 Novel Sequence

0400 155

Phe Asp Asp Tyr Gly His Leu Arg Phe
1 5

0210 156
0211 8
0212 PPT
0213 Artificial Sequence

0220
0223 Novel Sequence

0400 156

Met Asp Ser Asn Phe Ile Arg Phe
1 5

0210 157
0211 9
0212 PPT
0213 Artificial Sequence

0220
0223 Novel Sequence

0400 157

Phe Asp Asp Tyr Gly His Leu Arg Phe

1

5

<2110> 155
 <2111> 9
 <2112> PRT
 <2113> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 155

Phe Asp Asp Tyr Gly His Leu Arg Phe
 1 5

<210> 159
 <211> 9
 <2112> PRT
 <2113> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 159

Phe Asp Asp Tyr Gly His Met Arg Phe
 1 5

<210> 160
 <211> 14
 <2112> PRT
 <2113> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 160

Gly Gly Asp Asp Gln Phe Asp Asp Tyr Gly His Met Arg Phe
 1 5 10

<210> 161
 <211> 8
 <2112> PRT
 <2113> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 161

Ser Arg Pro Tyr Ser Phe Gly Leu
 1 5

<210> 162
 <211> 7
 <2112> PRT
 <2113> Artificial Sequence

<220>

<223> Novel Sequence

<400> 162

Asp Tyr Gly His Met Arg Phe
1 5

<210> 163

<211> 9

<212> PFT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 163

Ala Pro Arg Thr Pro Gly Gly Arg Arg
1 5

<210> 164

<211> 8

<212> PFT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 164

Val Glu Arg Tyr Ala Phe Gly Leu
1 5

<210> 165

<211> 8

<212> PFT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 165

Leu Pro Val Tyr Asn Phe Gly Leu
1 5

<210> 166

<211> 11

<212> PFT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 166

Thr Thr Arg Pro Gln Pro Phe Asn Phe Gly Leu
1 5 10

<210> 167

<211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 167

Glu Asp Val Asp His Val Phe Leu Arg Phe
 1 5 10

<210> 168
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Novel Sequence

<400> 168

Gly Asn Ser Phe Leu Arg Phe
 1 5